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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/828,217

DATE: 06/14/2001

TIME: 15:44:47

Input Set : N:\CrF3\RULE60\09828217.txt

Output Set: N:\CRF3\06142001\I828217.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: HIRANO, TOSHIO

6 KAISHO, TSUNEYASU

8 (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING

9 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF

11 (iii) NUMBER OF SEQUENCES: 2

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
15 P.C.

16 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

17 (C) CITY: ARLINGTON

18 (D) STATE: VA

19 (E) COUNTRY: USA

20 (F) ZIP: 22202

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/828,217

C--> 30 (B) FILING DATE: 09-Apr-2001

31 (C) CLASSIFICATION:

40 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/182,563

35 (B) FILING DATE:

37 (A) APPLICATION NUMBER: PCT/JP94/01732

38 (B) FILING DATE: 14-OCT-1994

41 (A) APPLICATION NUMBER: JP 5-281622

42 (B) FILING DATE: 15-OCT-1993

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: OBLON, NORMAN F.

46 (B) REGISTRATION NUMBER: 24,618

47 (C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 703-413-3000

51 (B) TELEFAX: 703-413-2220

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 180 amino acids

58 (B) TYPE: amino acid

59 (C) STRANDEDNESS: single

60 (D) TOPOLOGY: linear

62 (ii) MOLECULE TYPE: peptide

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

69 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

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70      1          5          10          15
72  Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
73                20                25                30
75  Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
76                35                40                45
78  Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
79                50                55                60
81  Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
82        65                70                75                80
84  Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
85                85                90                95
87  Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
88                100               105               110
90  Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
91                115               120               125
93  Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
94        130               135               140
96  Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
97        145               150               155               160
99  Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
100               165               170               175
102  Ala Leu Leu Gln
103               180
105 (2) INFORMATION FOR SEQ ID NO: 2:
107   (i) SEQUENCE CHARACTERISTICS:
108       (A) LENGTH: 996 base pairs
109       (B) TYPE: nucleic acid
110       (C) STRANDEDNESS: double
111       (D) TOPOLOGY: linear
113   (ii) MOLECULE TYPE: cDNA to mRNA
114   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120 GTGGAATTCA TGGCATCTAC TTCGTATGAC TATTGCAGAG TGCCCATGGA AGACGGGGAT      60
122 AAGCGCTGTA AGCTTCTGCT GGGGATAGGA ATTCTGGTGC TCCTGATCAT CGTGATTCTG      120
124 GGGGTGCCCT TGATTATCTT CACCATCAAG GCCAACAGCG AGGCCTGCCG GGACGGCCTT      180
126 CGGGCAGTGA TGGAGTGTCG CAATGTCACC CATCTCCTGC AACAAGAGCT GACCGAGGCC      240
128 CAGAAGGGCT TTCAGGATGT GGAGGCCCAG GCCGCCACCT GCAACCACAC TGTGATGGCC      300
130 CTAATGGCTT CCCTGGATGC AGAGAAGGCC CAAGGACAAA AGAAAGTGGA GGAGCTTGAG      360
132 GGAGAGATCA CTACATTAAA CCATAAGCTT CAGGACGCGT CTGCAGAGGT GGAGCGACTG      420
134 AGAAGAGAAA ACCAGGTCTT AAGCGTGAGA ATCGCGGACA AGAAGTACTA CCCAGCTCC      480
136 CAGGACTCCA GTCCTGCTGC GCGGCCCCAG CTGCTGATTG TGCTGCTGGG CCTCAGCGCT      540
138 CTGCTGCAGT GAGATCCCAG GAAGCTGGCA CATCTTGAA GGTCCGTCCT GCTCGGCTTT      600
140 TCGCTTGAAC ATTCCCTTGA TCTCATCAGT TCTGAGCGGG TCATGGGGCA ACACGGTTAG      660
142 CGGGGAGAGC ACGGGGTAGC CGGAGAAGGG CCTCTGGAGC AGGTCTGGAG GGGCCATGGG      720
144 GCAGTCCTGG GTGTGGGGAC ACAGTCGGGT TGACCCAGGG CTGTCTCCCT CCAGAGCCTC      780
146 CCTCCGGACA ATGAGTCCCC CCTCTTGTCT CCCACCCTGA GATTGGGCAT GGGGTGCGGT      840
148 GTGGGGGGCA TGTGCTGCCT GTTGTATATG GTTTTTTTTC CGGGGGGGGT TGCTTTTTTC      900
150 TGGGGTCTTT GAGCTCCAAA AAATAAACAC TTCCTTTGAG GGAGAGCAAA AAAAAAAAAA      960
152 AAAAAAAAAA AAAAAAAAAA AAAGAATTCC ACCACA                                996

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/828,217

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Input Set : N:\Crf3\RULE60\09828217.txt

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]